



Hybrid vigour and variability for key growth characters and yield in cashew (*Anacardium occidentale* L.)

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Abstract

Hybrid vigour and assessment of genetic variability for important growth characters and yield traits in cashew were studied in eight cashew hybrids. The analysis of variance for the phenotypic data for 12 characters revealed significant variation among the genotypes except for tree spread, flowering laterals per m², non-flowering laterals per m² and sex ratio. The highest nut weight was observed in H-125 (12.07 g) whereas the lowest was in H-2452 (5.08 g). The maximum nut yield was noticed in hybrid H-126 with 5.96 kg tree⁻¹ while NRCC Selection-2 recorded lowest with 0.53 kg tree⁻¹. The standard heterosis over two checks, bold nut check (NRCC Sel-2) and high yielding check (Bhaskara) and variability parameters such as genotypic coefficient of variation, phenotypic coefficient of variation, broad-sense heritability and genetic advance were estimated. For nut weight, standard heterosis over bold nut check varied from -34.54 to 55.54 per cent and six out of eight hybrids viz., H-43, H-66, H-68, H-125, H-126 and H-2473 showed significant and positive standard heterosis. Standard heterosis over the high yielding check, varied from -38.93 to 300 per cent and it was significant and positive in two hybrids viz., H-126 and H-125 with 300 per cent and 214.09 per cent, respectively. The hybrid vigour was not significant for trunk girth, tree height, tree spread, number of flowering laterals per m² and sex ratio. Notably, five hybrids presented more than 20 per cent standard heterosis for nut weight over bold nut check which may serve as a useful source of breeding material. Two hybrids viz., H-125 and H-126 showed good hybrid vigour for nut weight and yield over two checks and thus have been inducted into multi-location trials and also under consideration for release.

Keywords: Hybrid vigour, nut weight, standard heterosis, variability, yield

Introduction

Cashew is an important plantation crop grown mainly in tropical nations for its nuts and apples. It also gives a by-product namely cashewnut shell liquid (CNSL) having large industrial applications. Cashew kernels play a significant role as a source of protein and energy in human nutrition. There has been a growing demand for cashew in India as well as in other cashew growing countries. On the other hand, production and productivity are low due to many reasons. India ranks second in the world with respect to cashew growing area and production with 0.978 million ha and 0.745 million tons respectively. Yet, its yield levels are just above the world average (663 kg ha⁻¹) with 761.8 kg ha⁻¹ and far below the productivity of Vietnam with 3041.2 kg ha⁻¹ (FAOSTAT, 2017). The estimated demand for

India's raw cashewnut production is 21.9 lakh MT by the year 2025 (CEPCI, 2017).

In the above context, with an aim to improve productivity, Indian cashew breeding programs have been focusing on evolving high yielding varieties for different cashew growing regions in the country mainly through selection and heterosis breeding approaches. The heterosis, also called as hybrid vigour, is defined as the superior performance of the hybrid over its parents (Shull, 1914). The hybrid vigour may be in the form of an increase in growth and yield characters. It has been utilized greatly in many crops for increasing productivity. There are three types of heterosis viz., mid parent heterosis (superiority of F₁ over the mean value of two parents), heterobeltiosis (superiority of F₁ over the better parent) and standard heterosis (superiority of F₁

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over the standard commercial variety/check). Meredith and Bridge (1972) used the term “useful heterosis” for the “standard heterosis”. It is also called as “economic heterosis” as it has direct practical value in plant breeding. The importance of estimating it was advocated by Swaminathan *et al.* (1972). The hybrid vigour obtained in cashew can be capitalized and utilized directly through clonal propagation at any stage of the breeding program, which is an added advantage.

Though cashew was introduced to India by Portuguese in the 16th century, low, but considerable genetic diversity exists in Indian cashew (Archak *et al.*, 2009). Thus, there is ample scope for enriching the cashew genetic base in India through the introduction of wild species from Brazil, which houses many such species. Utilizing the existing genetic variability in India, many hybrids harnessing hybrid vigour have been developed for commercial production. However, studies on hybrid vigour for important growth characters and nut size and yield over local check variety are limited in cashew. The extent of genetic variability in any crop plays a crucial role in the success of the breeding method adopted for its improvement. However, genetic factors such as the number of genes and their action, broad-sense heritability and genetic advance influencing the inheritance of trait, decides the efficiency of the breeding method employed for the crop. In this context, the study of genetic variability parameters is indispensable for planning crop breeding activities. A few reports are available on the estimation of genetic variability parameters (Faluyi, 1987; Sena *et al.*, 1994; Lenka *et al.*, 2001; Reddy *et al.*, 2002) and heterosis in cashew (Cavalcanti *et al.*, 2000; Cavalcanti *et al.*, 2003;

Sankaranarayanan *et al.*, 2015; Kabita *et al.*, 2016). Therefore, an investigation on hybrid vigour and variability for key growth characters and yield in cashew was carried out.

Materials and methods

Experimental site

The experiment was laid out in the year 2006 at Kemminje campus of ICAR-Directorate of Cashew Research, Puttur (12.87°N latitude and 74.88°E longitude) in the Dakshina Kannada District of Karnataka. The soils are lateritic, and the annual average rainfall is 4000 mm in this region.

Experimental material

The experimental material consisted of eight promising hybrids of cashew and two popular local checks (Table 1). The important characteristic features of the parents used in the hybridization are presented in Table 2. The eight promising hybrids

Table 1. Details of F1 hybrids and check varieties

Sl. No.	Name of F1 hybrid	Parentage
1.	H-43	NRCC Sel-2 x Bhuthnath-II
2.	H-66	NRCC Sel-2 x Bhuthnath-II
3.	H-68	NRCC Sel-2 x Bhuthnath-II
4.	H-125	NRCC Sel-2 x Bedasi
5.	H-126	NRCC Sel-2 x Bedasi
6.	H-2452	VRI-2 x NRCC Sel-2
7.	H-2473	VRI-2 x NRCC Sel-2
8.	H-1250	BLA-139 x VTH-711/4
9.	NRCC Sel-2 (Bold nut check)	Selection from germplasm
10.	Bhaskara (Yield check)	Selection from germplasm

Table 2. Characteristic features of parents used in hybridization

Trait	NRCC Sel-2	Bhuthnath-II	Bhedasi	VRI-2	BLA-139-1	VTH-711/4
No. of nuts kg ⁻¹	108	108	100	195	168	65
Nut weight (g)	9.2	9.2	10.0	5.1	5.95	15.4
Kernel weight (g)	2.15	2.8	3.0	1.45	1.67	4.4
Shelling %	28.6	30.3	29.0	28.3	27.99	28.1
Export grade	W210	W210	W180	W280	W280	W180
Mean nut yield tree ⁻¹ (kg)	9.0	6.1	5.21	7.4	12.0	4.22
Apple colour	Pink	Yellow red	Yellow	Pinkish yellow	Pinkish yellow	Yellow

were selected from an initial evaluation trial of hybrid seedlings of various cross combinations planted at ICAR-DCR Experimental Station, Shantigodu, Puttur during the year 2000 from the data of eight consecutive harvests. First check (NRCC Sel-2) is a bold nut variety and is used as a bold nut check and second check (Bhaskara) is a popular high yielding variety. Both checks were developed and released by the ICAR-DCR, Puttur.

Experimental design and layout

All the genotypes were planted at 6 m x 6 m spacing in a randomized complete block design (RCBD) with three replications during 2006. There were three trees per genotype in each replication. Recommended horticultural practices and suitable control measures for weeds and insect pests were followed.

Phenotyping

The observations on growth characters like plant height (m), trunk girth (cm), the tree spread [(average of N-S and E-W directions (m))] were taken from the first year after planting. In contrast, observations on the number of flowering laterals per m², non-flowering laterals per m², sex ratio, nut weight (g), nut length (cm), nut width (cm), nut thickness (cm), shelling percentage and nut yield (kg tree⁻¹) were recorded from the 3rd year after planting as per the methodology described in the experimental manual on cashew by the National Research Center for Cashew (NRCC, 2005). The height of the tree was measured using marked bamboo pole/PVC pipe from the ground to the tip of the main branch in meters. The circumference of the trunk or main stem at the collar region (15 cm above ground level) was measured, using a measuring tape, in centimetres. The canopy spread in an east-west direction, and north-south direction was measured using a measuring tape and average of the two directions was expressed as tree spread in metres. The number of flowering laterals and non-flowering laterals were counted from one square meter area of the canopy in four directions, and the mean of four directions was taken. For calculating sex ratio, three panicles were selected from the observational tree and tagged. The numbers of bisexual and male flowers appearing in each panicle were counted on alternate days, and the counted

flowers were removed. This procedure was followed until the end of flowering in those panicles. The total number of bisexual and male flowers in each panicle was obtained. The mean of bisexual flowers per panicle and the mean of male flower per panicle was determined. The sex ratio was calculated as:

$$\text{Sex ratio} = \frac{\text{mean of bisexual flowres}}{\text{mean of male flowers}}$$

For nut weight, 50 raw nuts were sun-dried for three days, and weight was taken in grams. The mean weight of nut was calculated as:

$$\text{Nut weight} = \frac{\text{weight of 50 nuts}}{\text{number of nuts}}$$

The dimensions of nut such as length, width and thickness were measured by taking five randomly selected nuts in each genotype using digital callipers in centimetres. For shelling percentage, 50 raw nuts were weighed, and weight was taken in grams. These nuts were shelled using shelling machine. Weight of kernel with testa and weight of shells obtained after shelling were recorded separately. The shelling percentage was calculated as:

$$\text{Shelling percentage} = \frac{\text{weight of kernels with testa}}{\text{weight of nuts}} \times 100$$

For nut yield, nuts collected from each tree were sun-dried for three days and weighed for each genotype separately and expressed as nut yield per tree in kg.

Statistical analysis

The data of all the above observations recorded during the 5th harvest year were subjected for statistical analysis such as analysis of variance, and variability parameters like phenotypic and genotypic coefficients of variation, broad-sense heritability and genetic advance (Johnson *et al.*, 1955). The data was analyzed using WASP 2.0 (ICAR-CCARI, Goa) for randomized block design and further, variability parameters were calculated using MS-Excel 2007. From the analysis of variance table, environmental, genotypic and phenotypic variances were calculated as suggested by Lush (1940), and their coefficients

of variation were computed as suggested by Burton (1952). The values of phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were classified as low (<10%), moderate (10-20%) and high (>20%) (Sivasubramanian and Madhavamenon, 1973). The broad-sense heritability values were categorized as low (<30%), moderate (30-60%) and high (>60%) (Johnson *et al.*, 1955). The values of genetic advances per cent of mean were classified as low (<10%), moderate (10-20%) and high (>20%) (Johnson *et al.*, 1955). The standard heterosis, *i.e.*, heterosis over check variety for each trait, was calculated as:

$$\text{Standard heterosis} = \frac{\text{mean of hybrid} - \text{mean of check variety}}{\text{mean of check variety}} \times 100$$

$$\text{Standard heterosis} = \frac{\bar{F1} - \overline{SV}}{\overline{SV}} \times 100$$

Where, $\bar{F1}$ = mean of the trait in F1, \overline{SV} = mean of the trait in standard/check variety

The significance of standard heterosis was checked by calculating 't' value using the formula:

$$t = \frac{\bar{F1} - \overline{SV}}{SEd} \times 100$$

$$SEd = \sqrt{2EMS/r}$$

Then, calculated 't' value was compared with table 't' value at error df for its significance.

Results and discussion

The analysis of variance for 12 characters revealed significant variation among the genotypes evaluated in the study except for tree spread, flowering laterals per m², non-flowering laterals per m² and sex ratio (Table 3).

Per se performance of genotypes

The *per se* performance of all the genotypes evaluated is given in Table 4. The hybrid H-2452 recorded minimum tree height (4.53 m) while local check Bhaskara variety showed maximum height (6.37 m). The trunk girth was highest in Bhaskara variety (63.23 cm) and lowest in H-1250 (46.87 cm). The minimum tree spread was observed in the local check NRCC Selection-2 (4.87 m), and the maximum was in H-2473 (6.23 m). The highest nut weight was noticed in H-125 (12.07 g) whereas the lowest was in H-2452 (5.08 g). The minimum nut length was observed in H-1250 (3.03 cm), and the maximum was in H-43 (3.93 cm). The nut width was highest in H-43 (2.87 cm) and lowest in H-2452 (2.27 cm). The variety Bhaskara had minimum nut thickness (1.79 cm) whereas H-125 had maximum (2.47 cm). The hybrid H-1250 recorded the highest shelling percentage of 34.50 per cent, and the hybrid H-43 recorded lowest with 26.05 per cent. The hybrid H-126 gave the maximum nut yield with 5.96 kg tree⁻¹ while NRCC Selection-2 recorded lowest with 0.53 kg tree⁻¹.

Variability parameters

The variability parameters estimated for each character considering all the genotypes are presented in Table 5. Tree height recorded genotypic

Table 3. Analysis of variance for growth characters and nut yield

Trait / Parameter	Tree height (m)	Trunk girth (cm)	Tree spread (m)	Flowering laterals	Non-flowering laterals	Nut weight (g)	Nut length (cm)	Nut width (cm)	Nut thickness (cm)	Shelling percentage	Sex ratio	Nut yield (kg tree ⁻¹)
Mean squares (Genotypes)	0.949	96.810	0.606	3.127	9.349	16.056	0.293	0.135	0.233	21.005	0.078	9.130
Mean squares (Error)	0.298	31.395	0.695	2.455	7.817	0.054	0.010	0.008	0.005	1.945	0.032	1.033
F ratio	3.20 *	3.08 *	0.87	1.27	1.20	294.64 **	28.78 **	16.21 **	49.07 **	10.80 **	2.39	8.84 **
Probability	0.017	0.020	0.566	0.315	0.355	0.000	0.000	0.000	0.000	0.000	0.055	0.000

Table 'F' value at P = 0.05 for df ^(9, 18) = 2.46

*Where 9 = df due to genotypes and 18 = df due to error

Table 4. Per se performance of genotypes for growth characters and nut yield

Genotype/ Trait	Tree height (m)	Trunk girth (cm)	Tree spread (m)	Flowering laterals	Non- flowering laterals	Nut weight (g)	Nut length (cm)	Nut width (cm)	Nut thickness (cm)	Shelling percentage	Sex ratio	Nut yield (kg tree ⁻¹)
H-43	4.90	49.67	5.37	5.43	16.70	10.05	3.93	2.87	1.82	26.05	0.28	1.94
H-66	5.63	51.90	5.43	4.73	13.10	9.46	3.58	2.64	1.79	29.70	0.25	1.49
H-68	5.73	58.27	6.17	5.87	16.63	10.36	3.71	2.74	1.87	27.93	0.28	2.56
H-125	4.77	51.27	5.17	5.47	13.83	12.07	3.58	2.68	2.47	29.13	0.30	4.68
H126	5.27	57.17	5.43	5.07	14.63	11.33	3.66	2.69	2.40	29.10	0.20	5.96
H-1250	4.67	46.87	5.20	7.63	17.33	6.99	3.03	2.32	2.09	34.50	0.32	2.37
H-2452	4.53	50.10	5.97	4.50	16.57	5.08	3.04	2.27	1.64	30.15	0.61	0.91
H-2473	5.27	62.43	6.23	4.93	15.80	9.15	3.72	2.79	1.88	31.95	0.04	0.96
NRCC Sel-2	5.13	50.93	4.87	7.13	15.97	7.76	3.32	2.59	2.06	32.57	0.05	0.53
Bhaskara	6.37	63.23	5.50	5.30	12.07	5.91	3.17	2.33	1.72	33.61	0.17	1.49
Mean	5.23	54.18	5.53	5.61	15.26	0.25	8.81	3.47	2.59	30.47	0.25	2.29
SEm ±	0.18	1.8	0.14	0.90	1.61	0.13	0.10	0.07	0.09	0.84	0.10	0.55
CD (5%)	0.94	9.61	NS	2.69	4.79	0.40	0.17	0.16	0.12	2.39	0.31	1.74

coefficient of variation (GCV) of 8.90 per cent and phenotypic coefficient of variation (PCV) 13.74 per cent. The broad-sense heritability and genetic advance as a percentage of the mean (GAM) were 41.94 per cent and 11.87 per cent for this trait. Trunk girth presented a GCV of 8.62 per cent and PCV of 13.46 per cent and its broad sense heritability and GAM values were 40.98 per cent and 11.36 per cent. Tree spread showed GCV and PCV of 2.76 per cent and 15.38 per cent and broad-sense heritability and GAM values of 3.23 per cent and 1.02 per cent, respectively. The number of flowering laterals had GCV of 8.44 per cent and PCV of 29.19 per cent

while its broad sense heritability and GAM values were 8.36 per cent and 5.0 per cent.

On the other hand, for the number of non-flowering laterals the GCV and PCV values were 4.68 per cent, and 18.91 per cent and broad-sense heritability and GAM values were 6.13 per cent and 2.39 per cent. For sex ratio, GCV and PCV values were 49.28 per cent, and 87.49 per cent and broad-sense heritability and GAM values were 31.73 per cent and 57.19 per cent. Nut weight had GCV and PCV values of 26.20 per cent and 26.33 per cent and broad-sense heritability and GAM values of 98.99 per cent and 56.70 per cent,

Table 5. Variability estimates for growth characters and nut yield

Variable/ Trait	Tree height (m)	Trunk girth (cm)	Tree spread (m)	Flowering laterals	Non- flowering laterals	Sex ratio	Nut weight (g)	Nut length (cm)	Nut width (cm)	Nut thickness (cm)	Shelling percentage	Nut yield (kg tree ⁻¹)
Mean	5.23	54.18	5.53	5.61	15.26	0.25	8.81	3.47	2.59	1.97	30.47	2.29
Minimum	4.53	46.87	4.87	4.50	12.07	0.17	5.08	3.03	2.27	1.64	26.05	0.53
Maximum	6.37	63.23	6.23	7.63	17.33	0.61	12.07	3.93	2.87	2.47	34.50	5.96
Range	1.83	16.37	1.37	3.13	5.26	0.44	6.99	0.90	0.60	0.83	8.45	5.43
GCV (%)	8.90	8.62	2.76	8.44	4.68	49.28	26.20	8.80	7.88	13.75	8.27	71.75
PCV (%)	13.74	13.46	15.38	29.19	18.91	87.49	26.33	9.26	8.78	14.65	9.46	84.34
h ² _{bs} (%)	41.94	40.98	3.23	8.36	6.13	31.73	98.99	90.32	80.65	88.00	76.52	72.39
GA as % of mean (GAM)	11.87	11.36	1.02	5.02	2.39	57.19	56.70	17.24	14.58	26.56	14.91	125.76

Table 6. Standard heterosis among hybrids over check variety NRCC Sel-2 for growth and yield traits

Hybrid/ Trait	H-43		H-66		H-68		H-125		H-126		H-1250		H-2452		H-2473	
	St. H (%)	t val	St. H (%)	t val												
TG (cm)	-2.36	-0.26	1.96	0.22	14.54	1.62	0.79	0.09	12.38	1.38	-7.86	-0.87	-1.57	-0.17	2.59*	2.51
TH (m)	-4.48	-0.51	9.75	1.12	11.70	1.34	-7.02	-0.80	2.73	0.31	-8.97	-1.03	-11.70	-1.34	2.73	0.31
TS (m)	10.27	0.73	11.50	0.82	26.69	1.90	6.16	0.44	11.50	0.82	6.78	0.48	22.59	1.61	27.93	1.99
FLm ²	-23.84	-1.33	-33.66	-1.87	-17.67	-0.98	-23.28	-1.30	-28.89	-1.61	7.01	0.39	-36.89	-2.05	-30.86	-1.72
NFLm ²	4.57	0.32	-17.97	-1.26	4.13	0.29	-13.40	-0.94	-8.39	-0.59	8.52	0.60	3.76	0.26	-1.06	-0.07
SR	460.00	1.63	400.00	1.41	460.00	1.63	500.00	1.77	300.00	1.06	520.00	1.84	1120.0*	3.96	-20.00	-0.07
NW(g)	29.51*	12.54	21.91*	9.31	33.51*	14.24	55.54*	23.61	46.01*	19.55	-9.92	-4.22	-34.54	-14.68	17.91*	7.61
NL (cm)	18.36*	7.47	7.82*	3.18	11.5*	4.69	7.62*	3.10	10.03*	4.08	-8.83	-3.59	-8.43	-3.43	11.84*	4.82
NWI (cm)	10.54*	3.74	1.93	0.68	5.66	2.01	3.34	1.19	3.73	1.32	-10.41	-3.70	-12.60	-4.47	7.46*	2.65
NT (cm)	-11.35	-4.04	-12.97	-4.62	-8.91	-3.18	20.10*	7.16	16.86*	6.00	1.46	0.52	-20.26	-7.22	-8.43	-3.00
SH (%)	-20.0	-5.71	-8.81*	-2.52	-14.24	-4.07	-10.55	-3.01	-10.66	-3.04	5.94	1.70	-7.41	-2.12	-1.90	-0.54
Y (kg tree ⁻¹)	266.04	1.70	181.13	1.16	383.0*	2.45	783.0*	5.01	1024.5*	6.55	347.17*	2.22	71.70	0.46	81.13	0.52

St.H=Standard Heterosis; TG=Trunk girth; TH=Tree height; FL=Flowering laterals; NFL=Non-flowering laterals;NW=Nut weight; NL=Nut length; NWI: Nut width; NT=Nut thickness; SH=Shelling percentage; Y= Nut yield Table 't' value at Probability (P) =0.05 for df₁₈ = 2.101 * Indicates significance at Probability (P) =0.05

Table 7. Standard heterosis among hybrids over check variety Bhaskara for growth and yield traits

Hybrid/ Trait	H-43		H-66		H-68		H-125		H-126		H-1250		H-2452		H-2473	
	St. H (%)	t val														
TG (cm)	-21.36	-2.95	-17.88	-2.47	-7.75	-1.07	-18.83	-2.60	-9.49	-1.31	-25.79	-3.56	-20.73	-2.86	-1.27	-0.17
TH (m)	-23.08	-3.29	-11.62	-1.65	-10.05	-1.43	-25.12	-3.58	-17.27	-2.46	-26.69	-3.80	-28.89	-4.11	-17.27	-2.46
TS (m)	-2.36	-0.19	-1.27	-0.10	12.18	0.98	-6.00	-0.48	-1.27	-0.10	-5.45	-0.44	8.55	0.69	13.27	1.07
FL	2.45	0.10	-10.75	-0.45	10.75	0.45	3.21	0.13	-4.34	-0.18	43.96	1.82	-15.09	-0.62	-6.98	-0.29
NFL	38.36	2.03	8.53	0.45	37.78	2.00	14.58	0.77	21.21	1.12	43.58*	2.30	37.28	1.97	30.90	1.63
SR	64.71	0.78	47.06	0.57	64.71	0.78	76.47	0.92	17.65	0.21	82.35	0.99	258.82*	3.11	-76.47	-0.92
NW (g)	70.05*	22.68	60.07*	19.44	75.30*	24.37	104.23*	33.74	91.71*	29.69	18.27*	5.92	-14.04	-4.55	54.82*	17.75
NL (cm)	24.21*	9.39	13.16*	5.10	17.05*	6.61	12.95*	5.02	15.47*	6.00	-4.32	-1.67	-3.89	-1.51	17.37*	6.74
NWI (cm)	23.21*	7.39	13.61*	4.34	17.77*	5.66	15.19*	4.84	15.62*	4.98	-0.14	-0.05	-2.58	-0.82	19.77*	6.30
NT(cm)	5.80	1.73	3.87	1.15	8.70*	2.60	43.33*	12.93	39.46*	11.78	21.08*	6.29	-4.84	-1.44	9.28*	2.77
SH (%)	-22.48	-6.63	-11.64	-3.43	-16.90	-4.98	-13.33	-3.93	-13.43	-3.96	2.65	0.78	-10.28	-3.03	-4.95	-1.46
Y (kg tree ⁻¹)	30.20	0.54	0.00	0.00	71.81	1.29	214.09*	3.85	300.0*	5.39	59.06	1.06	-38.93	-0.70	-35.57	-0.64

St.H=Standard Heterosis; TG=Trunk girth; TH=Tree height; FL=Flowering laterals; NFL=Non-flowering laterals;NW=Nut weight; NL=Nut length; NWI: Nut width; NT=Nut thickness; SH=Shelling percentage; Y= Nut yield Table 't' value at Probability (P) =0.05 for df₁₈ = 2.101 * Indicates significance at Probability (P) =0.05

respectively. For nut length, GCV and PCV values were 8.80 per cent, and 9.26 per cent and broad-sense heritability and GAM values were 90.32 per cent and 17.24 per cent. Nut width revealed GCV of 7.88 per cent and PCV of 8.78 per cent and broad-sense heritability and GAM values of 80.65 per cent and 14.58 per cent. Values of GCV, PCV, broad-sense heritability and GAM were 13.75 per cent, 14.65 per cent, 88.00 per cent and 26.56 per cent for the nut thickness, respectively. Shelling percentage presented values of 8.27 per cent, 9.46 per cent, 76.52 per cent and 14.91 per cent for GCV, PCV, broad-sense heritability and GAM, respectively. In contrast, nut yield recorded 71.75 per cent, 84.34 per cent, 72.39 per cent and 125.76 per cent, respectively for the same.

In the present study, considerable variation was observed for the characters such as trunk girth, flowering and non-flowering laterals per m², nut weight, shelling percentage and nut yield as denoted by their range values. The hybrid H-2473 with highest values for trunk girth and H-125 for nut weight and H-1250 for flowering laterals per m² as well as shelling percentage could be used as potential sources of germplasm in future cashew breeding programmes. The hybrid H-126 manifested highest yield performance among the hybrids and checks with the additional advantage of bold nuts which can be used as a special trait and released as a variety.

The values of GCV were high for sex ratio, nut weight and nut yield tree⁻¹ demonstrating the genetic diversity for these traits in the genotypes used (as per the classification given by Sivasubramanian and Madhavamenon, 1973). Besides, these characters showed moderate (sex ratio) to high broad-sense heritability coupled with high GAM indicating the involvement of additive gene action for their expression and useful for selection (as per the classification given by Johnson *et al.*, 1955). Similar results were obtained by Faluyi (1987) and Lenka *et al.* (2001) for nut yield tree⁻¹ and Reddy *et al.* (2002) for nut weight. However, Sena *et al.* (1994) reported high values of GCV, broad-sense heritability and GAM for sex ratio. It was observed that the difference between estimates of GCV and PCV were narrow for nut characters such as weight, length, width and thickness and shelling percentage.

The results agree with Faluyi (1987), who reported GCV over 50 per cent of the PCV for eight nut traits. This implies that these characters had less sensitivity to environment and variation observed in these characters has a genetic basis. Hence, PCV can be a reliable measure of genetic variability for these characters. Besides, nut length, nut width and shelling percentage showed high broad sense heritability coupled with moderate GAM whereas, nut thickness had high broad sense heritability coupled with high GAM denoting influence of additive gene action for their expression and advantage for selection. However, higher differences in PCV and GCV were observed for tree height, trunk girth, tree spread, flowering and non-flowering laterals perm² indicating the role of environment on the expression of these characters. Moderate broad sense heritability coupled with moderate GAM values were obtained for tree height and trunk girth implying additive gene action governing their expression and a considerable chance for selection. Whereas, low, broad sense heritability coupled with low GAM values were obtained for tree spread, flowering and non-flowering laterals perm² indicating the high influence of environment and a bleak chance for selection. Contrasting results were observed by Reddy *et al.* (2002) for flowering shoots per m².

Standard heterosis: Hybrid vigour

The magnitude of standard heterosis or hybrid vigour over the two local check varieties estimated for the traits is presented in Table 6 (for NRCC Sel-2) and Table 7 (for Bhaskara).

Standard heterosis over NRCC Sel-2 (Bold nut check)

The standard heterosis over the check NRCC Sel-2 for the traits such as tree height, tree spread, number of flowering laterals and number of non-flowering laterals was not significant among all the eight hybrids tested. For the trunk girth, standard heterosis varied from -7.86 per cent to 14.54 per cent, and it was significant and positive only in the hybrid H-2473 with 2.59 per cent. In the case of sex ratio, it ranged from -20 per cent to 1120 per cent and was significant and positive only in the hybrid H-2452 with 1120 per cent. For nut weight and nut length, six out of eight hybrids *viz.*, H-43, H-66,

H-68, H-125, H-126 and H-2473 showed significant and positive standard heterosis. Standard heterosis varied from -34.54 per cent to 55.54 per cent and -8.83 per cent to 18.36 per cent in case of nut weight and nut length, respectively. For nut width, standard heterosis varied from -12.60 per cent to 10.54 per cent, and it was significant and positive in two hybrids *viz.*, H-43 and H-2473 with 10.54 per cent and 7.46 per cent, respectively. For nut thickness, standard heterosis varied from -20.20 per cent to 20.10 per cent, and it was significant and positive in two hybrids *viz.*, H-125 and H-126 with 20.10 per cent and 16.86 per cent, respectively. For shelling percentage, standard heterosis varied from -20 per cent to 5.94 per cent, and it was significant and negative in the hybrid H-66 with -8.81 per cent. For nut yield, standard heterosis varied from 71.70 per cent to 1024.50 per cent, and it was significant

and positive in four hybrids *viz.*, H-126, H-125, H-68 and H-1250 with 1024.50 per cent, 783 per cent, 383 per cent and 347.07 per cent, respectively.

Standard heterosis over Bhaskara (High yield check)

The standard heterosis over the local high yielding check, Bhaskara, for the traits such as trunk girth, tree height, tree spread and the number of flowering laterals was not significant among all the eight hybrids tested. For the number of non-flowering laterals, standard heterosis varied from 8.53 per cent to 43.58 per cent, and it was significant and positive only in the hybrid H-1250 with 43.58 per cent. In the case of sex ratio, it ranged from -76.47 to 258.82 per cent. The maximum heterosis obtained for this trait was significant and positive in the hybrid H-2452. For nut weight, standard



H-126 (Hybrid)



H-125 (Hybrid)



NRCC Sel-2 (Check)



Bhaskara (Check)

Fig. 1. The fruiting clusters of hybrids (top row) showing hybrid vigour for nut size over checks (bottom row)

heterosis varied from -14.04 (H-2452) to 104.23 per cent (H-125), and it was significant and positive in seven out of eight hybrids *viz.* H-43, H-66, H-68, H-125, H-126, H-1250 and H-2473. For nut length and nut width, six out of eight hybrids *viz.*, H-43, H-66, H-68, H-125, H-126 and H-2473 showed significant and positive standard heterosis. Standard heterosis varied from -4.32 per cent (H-1250) to 24.21 per cent (H-43) and -0.14 per cent (H-1250) to 23.21 per cent (H-43) in nut length and nut width, respectively. For nut thickness, standard heterosis varied from -4.84 per cent (H-2452) to 43.33 per cent (H-125), and it was significant and positive in five hybrids *viz.*, H-68, H-125, H-126, H-1250 and H-2473. For shelling percentage, standard heterosis varied from -22.48 per cent (H-43) to 2.65 per cent (H-1250) and seven hybrids showed negative and non-significant standard heterosis and one hybrid showed positive but non-significant standard heterosis. For nut yield, standard heterosis varied from -38.93 per cent (H-2452) to 300 per cent (H-126), and it was significant and positive in two hybrids *viz.*, H-126 and H-125 with 300 per cent and 214.09 per cent, respectively (Fig.1). The standard heterosis for yield was zero in the case of H-66.

As cashew is highly heterozygous and cross-pollinated species, hybridization between clones results in segregating progenies and each seedling progeny is basically a hybrid. Therefore, all the individuals generated behave akin to F_2 generation wherein selection should be exercised immediately for fixing the hybrid vigour in cross combinations (Barros *et al.*, 1999). Accordingly, in the present study, eight hybrids were selected from the crosses; clones were multiplied and evaluated in a replicated trial. The estimated standard heterosis or hybrid vigour in hybrids varied among the characters perhaps due to artificial selection, and it is favoured for the traits to yield. In our study, the standard heterosis was not significant for trunk girth, tree height, tree spread, number of flowering laterals per m^2 and sex ratio in most of the hybrids tested over the two checks. This might be due to narrow genetic differences among the parents for these characters. But, significant and positive standard heterosis for these characters would be desirable as they are reported as positively correlated to nut yield (Manoj

et al., 1994; Rao *et al.*, 2002; Abraham *et al.*, 2007; Mohana *et al.*, 2015). The local variety NRCC Sel-2 was used as bold nut check as its nuts weigh 9.2 g. In the present study, five hybrids presented more than 20 per cent standard heterosis over this check which may serve as a useful source of breeding material. Bold nuts give higher kernel grades which in turn fetch a premium price for the processors. Most of the hybrids presented negative standard heterosis for shelling percentage over the two checks, which is undesirable. The shelling percentage, which is also called as kernel recovery percentage, is a very important trait from the point of processing of cashewnuts. The local variety Bhaskara was used as a check for nut yield as it yields about 10 kg per tree at the age of 10 years. Two hybrids, namely H-125 and H-126, could present significant and positive standard heterosis for nut yield over this check. These two hybrids are considered as unique types in showing hybrid vigour for nut weight as well as yield and are being conserved in the national cashew field gene bank.

In a similar line of work, Cavalcanti *et al.* (2000) reported average heterosis value of 20 per cent for plant height, 31.93 per cent for crown diameter, 120.77 per cent for nut number, 192.25 per cent for nut yield, 14.69 per cent for nut weight in the common cashew hybrids. Cavalcanti *et al.* (2003) reported heterosis values from -13.50 per cent to 43.60 per cent for plant height and -7.47 per cent to 60.27 per cent for crown diameter, from -45.85 per cent to 321.22 per cent for the number of nuts per plant; -50.35 per cent to 348.87 per cent for nut yield and from -16.34 per cent to 13.93 per cent for nut weight and their average values were 12.09 per cent, 19.38 per cent, 98.01 per cent, 96.97 per cent and -2.11 per cent indicating the presence of hybrid vigour in crosses between parents of early dwarf cashew trees, for all characters, except for nut weight. Kabita *et al.* (2016) reported comparable values of standard heterosis ranging from 15.51 per cent to 30.70 per cent for nut yield and -0.27 per cent to 19.68 per cent for nut weight in the 10-year-old 20 cashew hybrids. Results obtained in this study revealed that the hybridization has resulted in heterosis for the traits like nut weight, nut length

and nut yield, which can be exploited through clonal selection. The two hybrids H-125 and H-126 which were found promising for nut yield and nut weight have been recommended for multi-location trial on bold nut types in different cashew growing states of India.

Conclusions

Significant hybrid vigour was not obtained for the characters such as trunk girth, tree height, tree spread, number of flowering laterals per m² and sex ratio in most of the hybrids tested over the two checks. Five hybrids presented more than 20 per cent standard heterosis for nut weight over bold nut check NRCC Sel-2 which may serve as a useful source of breeding material. Most of the hybrids presented negative standard heterosis for shelling percentage over the two checks, which is undesirable. Two hybrids, namely H-125 and H-126, presented favourable hybrid vigour for nut weight as well as nut yield over two popular local checks which may be used as such or form the good source of germplasm. Considering the merits, H-125 and H-126 have been recommended for multi-location trial (MLT) on bold nut types in All India Coordinated Research Project (AICRP) on cashew to assess their performance in different cashew growing states of India.

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